

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
 Hannah, L. Curtis
 Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<150> US 60/496,188

<151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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 Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
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 Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
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Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys

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| Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn | | |
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| Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu | | |
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| Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp | | |
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| Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile | | |
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| Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg | | |
| 420 | 425 | 430 |
| Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala | | |
| 435 | 440 | 445 |
| Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val | | |
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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
          50          55          60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65          70          75          80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
          85          90          95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
          100          105          110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
          115          120          125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
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Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn

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| Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu | 195 | 200 | 205 |
| Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro | 210 | 215 | 220 |
| Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly | 225 | 230 | 235 |
| Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly | 245 | 250 | 255 |
| Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln | 260 | 265 | 270 |
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| Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu | 290 | 295 | 300 |
| Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr | 305 | 310 | 315 |
| Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile | 325 | 330 | 335 |
| Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp | 340 | 345 | 350 |
| Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys | 355 | 360 | 365 |
| Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala | 370 | 375 | 380 |
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| Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile | 405 | 410 | 415 |
| Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg | 420 | 425 | 430 |
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| Met | Asp | Met | Ala | Leu | Ala | Ser | Lys | Ala | Ser | Pro | Pro | Pro | Trp | Asn | Ala | 1 | 5 | 10 | 15 |
| Thr | Ala | Ala | Glu | Gln | Pro | Ile | Pro | Lys | Arg | Asp | Lys | Ala | Ala | Ala | Asn | 20 | 25 | 30 | |
| Asp | Ser | Glu | Thr | Cys | Leu | Asn | Pro | Gln | Ala | His | Asp | Ser | Val | Leu | Gly | 35 | 40 | 45 | |
| Ile | Ile | Leu | Gly | Gly | Gly | Ala | Gly | Thr | Arg | Leu | Tyr | Pro | Leu | Thr | Lys | 50 | 55 | 60 | |
| Lys | Arg | Ala | Lys | Pro | Ala | Val | Pro | Leu | Gly | Ala | Asn | Tyr | Arg | Leu | Ile | 65 | 70 | 75 | 80 |
| Asp | Ile | Pro | Val | Ser | Asn | Cys | Leu | Asn | Ser | Asn | Ile | Ser | Lys | Ile | Tyr | 85 | 90 | 95 | |
| Val | Leu | Thr | Gln | Phe | Asn | Ser | Ala | Ser | Leu | Asn | Arg | His | Leu | Ser | Arg | 100 | 105 | 110 | |
| Ala | Tyr | Gly | Ser | Asn | Ile | Gly | Gly | Tyr | Lys | Asn | Glu | Gly | Phe | Val | Glu | 115 | 120 | 125 | |
| Val | Leu | Ala | Ala | Gln | Gln | Ser | Pro | Asp | Asn | Pro | Asn | Trp | Phe | Gln | Gly | 130 | 135 | 140 | |
| Thr | Ala | Asp | Ala | Val | Arg | Gln | Tyr | Leu | Trp | Leu | Phe | Glu | Glu | His | Asn | 145 | 150 | 155 | 160 |
| Val | Met | Glu | Phe | Leu | Ile | Leu | Ala | Gly | Asp | His | Leu | Tyr | Arg | Met | Asp | 165 | 170 | 175 | |
| Tyr | Glu | Lys | Phe | Ile | Gln | Ala | His | Arg | Glu | Thr | Asn | Ala | Asp | Ile | Thr | 180 | 185 | 190 | |
| Val | Ala | Ala | Leu | Pro | Met | Asp | Glu | Lys | Arg | Ala | Thr | Ala | Phe | Gly | Leu | 195 | 200 | 205 | |
| Met | Lys | Ile | Asp | Glu | Glu | Gly | Arg | Ile | Ile | Glu | Phe | Ala | Glu | Lys | Pro | 210 | 215 | 220 | |
| Lys | Gly | Glu | Gln | Leu | Lys | Ala | Met | Met | Val | Asp | Thr | Thr | Ile | Leu | Gly | 225 | 230 | 235 | 240 |
| Leu | Asp | Asp | Val | Arg | Ala | Lys | Glu | Met | Pro | Tyr | Ile | Ala | Ser | Met | Gly | | | | |

| 245 | | | | | | | | | | 250 | | | | | 255 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Ile | Tyr | Val | Phe | Ser | Lys | Asp | Val | Met | Leu | Gln | Leu | Leu | Arg | Glu | Gln | | | | |
| | | | 260 | | | | | 265 | | | | | | 270 | | | | | |
| Phe | Pro | Glu | Ala | Asn | Asp | Phe | Gly | Ser | Glu | Val | Ile | Pro | Gly | Ala | Thr | | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | | |
| Ser | Ile | Gly | Lys | Arg | Val | Gln | Ala | Tyr | Leu | Tyr | Asp | Gly | Tyr | Trp | Glu | | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | | |
| Asp | Ile | Gly | Thr | Ile | Ala | Ala | Phe | Tyr | Asn | Ala | Asn | Leu | Gly | Ile | Thr | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | |
| Lys | Lys | Pro | Ile | Pro | Asp | Phe | Ser | Phe | Tyr | Asp | Arg | Phe | Ala | Pro | Ile | | | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | | | |
| Tyr | Thr | Gln | Pro | Arg | His | Leu | Pro | Pro | Ser | Lys | Val | Leu | Asp | Ala | Asp | | | | |
| | | | 340 | | | | | 345 | | | | | | 350 | | | | | |
| Val | Thr | Asp | Ser | Val | Ile | Gly | Glu | Gly | Cys | Val | Ile | Lys | Asn | Cys | Lys | | | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | | | |
| Ile | Asn | His | Ser | Val | Val | Gly | Leu | Arg | Ser | Cys | Ile | Ser | Glu | Gly | Ala | | | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | | | |
| Ile | Ile | Glu | Asp | Ser | Leu | Leu | Met | Gly | Ala | Asp | Tyr | Tyr | Glu | Thr | Glu | | | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | | | |
| Ala | Asp | Lys | Lys | Leu | Leu | Ala | Glu | Lys | Gly | Gly | Ile | Pro | Ile | Gly | Ile | | | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | | | |
| Gly | Lys | Asn | Ser | Cys | Ile | Arg | Arg | Ala | Ile | Ile | Asp | Lys | Asn | Ala | Arg | | | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | | | |
| Ile | Gly | Asp | Asn | Val | Lys | Ile | Leu | Asn | Ala | Asp | Asn | Val | Gln | Glu | Ala | | | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | | | |
| Ala | Met | Glu | Thr | Asp | Gly | Tyr | Phe | Ile | Lys | Gly | Gly | Ile | Val | Thr | Val | | | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | | | |
| Ile | Lys | Asp | Ala | Leu | Leu | Pro | Ser | Gly | Thr | Val | Ile | | | | | | | | |
| 465 | | | | | 470 | | | | | 475 | | | | | | | | | |

<210> 11

<211> 1582

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 11

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      Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
           35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
           50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
           65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
           80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
           95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
           115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
           130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
           145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu

```

| 160 | 165 | 170 | |
|---|-----|-----|------|
| gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | | | 579 |
| Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | | | |
| 175 | 180 | 185 | 190 |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | | | 627 |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | | | |
| | 195 | 200 | 205 |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | | | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | | | |
| | 210 | 215 | 220 |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | | | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | | | |
| | 225 | 230 | 235 |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | | | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | | | |
| | 240 | 245 | 250 |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | | | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | | | |
| | 255 | 260 | 265 |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | | | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | | | |
| | 275 | 280 | 285 |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | | | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | | | |
| | 290 | 295 | 300 |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | | | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | | | |
| | 305 | 310 | 315 |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cat agt | | | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser | | | |
| | 320 | 325 | 330 |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | | | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | | | |
| | 335 | 340 | 345 |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | | | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | | | |
| | 355 | 360 | 365 |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | | | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | | | |
| | 370 | 375 | 380 |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | | | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | | | |
| | 385 | 390 | 395 |

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca 1539
 Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
 495 500 505 510

acc atc aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1582
 Thr Ile Asn Asp Gly Ser Val Ile
 515

<210> 12

<211> 518

<212> PRT

<213> Zea mays

<400> 12

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile

1

5

10

15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
 485 490 495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 500 505 510

Asn Asp Gly Ser Val Ile

515

<210> 13

<211> 1582

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be
 heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 13

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1

5

10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50

55

60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65

70

75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly

80

85

90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

95

100

105

110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387

Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

115

120

125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435

Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130

135

140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn

145

150

155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531

Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu

160

165

170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579

Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe

175

180

185

190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627

Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile

195

200

205

| | |
|---|------|
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | |
| 210 215 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | |
| 225 230 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | |
| 240 245 250 | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |
| 415 420 425 430 | |

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca 1539
 Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
 495 500 505 510

acc atc aac gat ggg tct gtc ata tagatcggct gcgktgtcg 1582
 Thr Ile Asn Asp Gly Ser Val Ile
 515

<210> 14

<211> 518

<212> PRT

<213> Zea mays

<400> 14

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu

| 130 | 135 | 140 |
|---|-----|---------|
| Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala | | |
| 145 | 150 | 155 160 |
| Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro | | |
| | 165 | 170 175 |
| Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp | | |
| | 180 | 185 190 |
| Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile | | |
| | 195 | 200 205 |
| Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln | | |
| | 210 | 215 220 |
| Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val | | |
| 225 | 230 | 235 240 |
| Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr | | |
| | 245 | 250 255 |
| Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn | | |
| | 260 | 265 270 |
| Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala | | |
| | 275 | 280 285 |
| Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys | | |
| | 290 | 295 300 |
| Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp | | |
| 305 | 310 | 315 320 |
| Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln | | |
| | 325 | 330 335 |
| Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser | | |
| | 340 | 345 350 |
| Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp | | |
| | 355 | 360 365 |
| Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro | | |
| | 370 | 375 380 |
| Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp | | |
| 385 | 390 | 395 400 |
| Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val | | |
| | 405 | 410 415 |
| Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met | | |
| | 420 | 425 430 |
| Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu | | |

435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
 485 490 495
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 500 505 510
 Asn Asp Gly Ser Val Ile
 515

<210> 15
 <211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunken-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

<400> 15
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

| | |
|---|-----|
| agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt | 147 |
| Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe | |
| 35 40 45 | |
| ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct | 195 |
| Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala | |
| 50 55 60 | |
| tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat | 243 |
| Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr | |
| 65 70 75 | |
| gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga | 291 |
| Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly | |
| 80 85 90 | |
| tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct | 339 |
| Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro | |
| 95 100 105 110 | |
| gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc | 387 |
| Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe | |
| 115 120 125 | |
| aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act | 435 |
| Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr | |
| 130 135 140 | |
| tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac | 483 |
| Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn | |
| 145 150 155 | |
| ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa | 531 |
| Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu | |
| 160 165 170 | |
| gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | 579 |
| Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | |
| 175 180 185 190 | |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | 627 |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | |
| 195 200 205 | |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | |
| 210 215 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | |
| 225 230 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | |
| 240 245 250 | |

| | |
|---|------|
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |
| 415 420 425 430 | |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | |
| 435 440 445 | |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile | |
| 450 455 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | |
| 465 470 475 | |

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgctg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 16

<211> 516

<212> PRT

<213> Zea mays

<400> 16

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile

| 195 | | | | | 200 | | | | | 205 | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ser | Gly | Asp | Gln | Leu | Tyr | Arg | Met | Asn | Tyr | Met | Glu | Leu | Val | Gln | |
| 210 | | | | | 215 | | | | | 220 | | | | | | |
| Lys | His | Val | Glu | Asp | Asp | Ala | Asp | Ile | Thr | Ile | Ser | Cys | Ala | Pro | Val | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Asp | Glu | Ser | Arg | Ala | Ser | Lys | Asn | Gly | Leu | Val | Lys | Ile | Asp | His | Thr | |
| 245 | | | | | 250 | | | | | 255 | | | | | | |
| Gly | Arg | Val | Leu | Gln | Phe | Phe | Glu | Lys | Pro | Lys | Gly | Ala | Asp | Leu | Asn | |
| 260 | | | | | 265 | | | | | 270 | | | | | | |
| Ser | Met | Arg | Val | Glu | Thr | Asn | Phe | Leu | Ser | Tyr | Ala | Ile | Asp | Asp | Ala | |
| 275 | | | | | 280 | | | | | 285 | | | | | | |
| Gln | Lys | Tyr | Pro | Tyr | Leu | Ala | Ser | Met | Gly | Ile | Tyr | Val | Phe | Lys | Lys | |
| 290 | | | | | 295 | | | | | 300 | | | | | | |
| Asp | Ala | Leu | Leu | Asp | Leu | Leu | Lys | Ser | Lys | Tyr | Thr | Gln | Leu | His | Asp | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Phe | Gly | Ser | Glu | Ile | Leu | Pro | Arg | Ala | Val | Leu | Asp | Tyr | Ser | Val | Gln | |
| 325 | | | | | 330 | | | | | 335 | | | | | | |
| Ala | Cys | Ile | Phe | Thr | Gly | Tyr | Trp | Glu | Asp | Val | Gly | Thr | Ile | Lys | Ser | |
| 340 | | | | | 345 | | | | | 350 | | | | | | |
| Phe | Phe | Asp | Ala | Asn | Leu | Ala | Leu | Thr | Glu | Gln | Pro | Ser | Lys | Phe | Asp | |
| 355 | | | | | 360 | | | | | 365 | | | | | | |
| Phe | Tyr | Asp | Pro | Lys | Thr | Pro | Phe | Phe | Thr | Ala | Pro | Arg | Cys | Leu | Pro | |
| 370 | | | | | 375 | | | | | 380 | | | | | | |
| Pro | Thr | Gln | Leu | Asp | Lys | Cys | Lys | Met | Lys | Tyr | Ala | Phe | Ile | Ser | Asp | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Gly | Cys | Leu | Leu | Arg | Glu | Cys | Asn | Ile | Glu | His | Ser | Val | Ile | Gly | Val | |
| 405 | | | | | 410 | | | | | 415 | | | | | | |
| Cys | Ser | Arg | Val | Ser | Ser | Gly | Cys | Glu | Leu | Lys | Asp | Ser | Val | Met | Met | |
| 420 | | | | | 425 | | | | | 430 | | | | | | |
| Gly | Ala | Asp | Ile | Tyr | Glu | Thr | Glu | Glu | Glu | Ala | Ser | Lys | Leu | Leu | Leu | |
| 435 | | | | | 440 | | | | | 445 | | | | | | |
| Ala | Gly | Lys | Val | Pro | Val | Gly | Ile | Gly | Arg | Asn | Thr | Lys | Ile | Arg | Asn | |
| 450 | | | | | 455 | | | | | 460 | | | | | | |
| Cys | Ile | Ile | Asp | Met | Asn | Ala | Arg | Ile | Gly | Lys | Asn | Val | Val | Ile | Thr | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Asn | Ser | Lys | Gly | Ile | Gln | Glu | Ala | Asp | His | Pro | Glu | Glu | Gly | Tyr | Tyr | |
| 485 | | | | | 490 | | | | | 495 | | | | | | |
| Ile | Arg | Ser | Gly | Ile | Val | Val | Ile | Leu | Lys | Asn | Ala | Thr | Ile | Asn | Asp | |

500

505

510

Gly Ser Val Ile
515

<210> 17

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 17

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

| 50 | 55 | 60 | |
|---|-----|-----|-----|
| tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat | | | 243 |
| Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr | | | |
| 65 | 70 | 75 | |
| gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga | | | 291 |
| Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly | | | |
| 80 | 85 | 90 | |
| tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct | | | 339 |
| Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro | | | |
| 95 | 100 | 105 | 110 |
| ggt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc | | | 387 |
| Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe | | | |
| 115 | 120 | 125 | |
| aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act | | | 435 |
| Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr | | | |
| 130 | 135 | 140 | |
| tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac | | | 483 |
| Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn | | | |
| 145 | 150 | 155 | |
| ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa | | | 531 |
| Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu | | | |
| 160 | 165 | 170 | |
| gag cca ccn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | | | 579 |
| Glu Pro Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | | | |
| 175 | 180 | 185 | 190 |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | | | 627 |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | | | |
| 195 | 200 | 205 | |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | | | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | | | |
| 210 | 215 | 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | | | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | | | |
| 225 | 230 | 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | | | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | | | |
| 240 | 245 | 250 | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | | | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | | | |
| 255 | 260 | 265 | 270 |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | | | 867 |

| | |
|---|------|
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |
| 415 420 425 430 | |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | |
| 435 440 445 | |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile | |
| 450 455 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | |
| 465 470 475 | |
| atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg | 1491 |
| Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly | |
| 480 485 490 | |
| tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc | 1539 |

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgtcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 18
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 18

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val

| | | | |
|---|---|-----|-----|
| 225 | 230 | 235 | 240 |
| Asp Glu Ser Arg | Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr | | |
| | 245 | 250 | 255 |
| Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn | | | |
| | 260 | 265 | 270 |
| Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala | | | |
| | 275 | 280 | 285 |
| Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys | | | |
| | 290 | 295 | 300 |
| Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp | | | |
| 305 | 310 | 315 | 320 |
| Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln | | | |
| | 325 | 330 | 335 |
| Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser | | | |
| | 340 | 345 | 350 |
| Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp | | | |
| | 355 | 360 | 365 |
| Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro | | | |
| | 370 | 375 | 380 |
| Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp | | | |
| 385 | 390 | 395 | 400 |
| Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val | | | |
| | 405 | 410 | 415 |
| Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met | | | |
| | 420 | 425 | 430 |
| Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu | | | |
| | 435 | 440 | 445 |
| Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn | | | |
| | 450 | 455 | 460 |
| Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr | | | |
| 465 | 470 | 475 | 480 |
| Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr | | | |
| | 485 | 490 | 495 |
| Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp | | | |
| | 500 | 505 | 510 |
| Gly Ser Val Ile | | | |
| | 515 | | |

<210> 19
 <211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1209)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1371)
 <223> h = a or c or t/u.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

| | |
|---|-----|
| tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat | 243 |
| Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr | |
| 65 70 75 | |
| gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga | 291 |
| Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly | |
| 80 85 90 | |
| tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct | 339 |
| Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro | |
| 95 100 105 110 | |
| gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc | 387 |
| Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe | |
| 115 120 125 | |
| aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act | 435 |
| Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr | |
| 130 135 140 | |
| tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac | 483 |
| Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn | |
| 145 150 155 | |
| ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa | 531 |
| Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu | |
| 160 165 170 | |
| gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | 579 |
| Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | |
| 175 180 185 190 | |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | 627 |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | |
| 195 200 205 | |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | |
| 210 215 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | |
| 225 230 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | |
| 240 245 250 | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |

| 275 | 280 | 285 | |
|---|-----|-----|------|
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | | | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | | | |
| 290 | 295 | 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | | | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | | | |
| 305 | 310 | 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt | | | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser | | | |
| 320 | 325 | 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | | | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | | | |
| 335 | 340 | 345 | 350 |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | | | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | | | |
| 355 | 360 | 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | | | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | | | |
| 370 | 375 | 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | | | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | | | |
| 385 | 390 | 395 | |
| tca cay ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | | | 1251 |
| Ser His Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | | | |
| 400 | 405 | 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | | | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | | | |
| 415 | 420 | 425 | 430 |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | | | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | | | |
| 435 | 440 | 445 | |
| ctg tta gct ggg aag gtc ccr ath gga ata gga agg aac aca aag ata | | | 1395 |
| Leu Leu Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile | | | |
| 450 | 455 | 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | | | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | | | |
| 465 | 470 | 475 | |
| atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg | | | 1491 |
| Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly | | | |
| 480 | 485 | 490 | |
| tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc | | | 1539 |
| Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile | | | |

495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576

Asn Asp Gly Ser Val Ile

515

<210> 20
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 20

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 | | 230 | | 235 | | 240 | | | | | | | | | |
| Asp | Glu | Ser | Arg | Ala | Ser | Lys | Asn | Gly | Leu | Val | Lys | Ile | Asp | His | Thr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Gly | Arg | Val | Leu | Gln | Phe | Phe | Glu | Lys | Pro | Lys | Gly | Ala | Asp | Leu | Asn |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ser | Met | Arg | Val | Glu | Thr | Asn | Phe | Leu | Ser | Tyr | Ala | Ile | Asp | Asp | Ala |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Gln | Lys | Tyr | Pro | Tyr | Leu | Ala | Ser | Met | Gly | Ile | Tyr | Val | Phe | Lys | Lys |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asp | Ala | Leu | Leu | Asp | Leu | Leu | Lys | Ser | Lys | Tyr | Thr | Gln | Leu | His | Asp |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Phe | Gly | Ser | Glu | Ile | Leu | Pro | Arg | Ala | Val | Leu | Asp | His | Ser | Val | Gln |
| | | | 325 | | | | | | 330 | | | | | 335 | |
| Ala | Cys | Ile | Phe | Thr | Gly | Tyr | Trp | Glu | Asp | Val | Gly | Thr | Ile | Lys | Ser |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Phe | Phe | Asp | Ala | Asn | Leu | Ala | Leu | Thr | Glu | Gln | Pro | Ser | Lys | Phe | Asp |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Phe | Tyr | Asp | Pro | Lys | Thr | Pro | Phe | Phe | Thr | Ala | Pro | Arg | Cys | Leu | Pro |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Pro | Thr | Gln | Leu | Asp | Lys | Cys | Lys | Met | Lys | Tyr | Ala | Phe | Ile | Ser | His |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Gly | Cys | Leu | Leu | Arg | Glu | Cys | Asn | Ile | Glu | His | Ser | Val | Ile | Gly | Val |
| | | | 405 | | | | | | 410 | | | | | 415 | |
| Cys | Ser | Arg | Val | Ser | Ser | Gly | Cys | Glu | Leu | Lys | Asp | Ser | Val | Met | Met |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Gly | Ala | Asp | Ile | Tyr | Glu | Thr | Glu | Glu | Glu | Ala | Ser | Lys | Leu | Leu | Leu |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Ala | Gly | Lys | Val | Pro | Ile | Gly | Ile | Gly | Arg | Asn | Thr | Lys | Ile | Arg | Asn |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Cys | Ile | Ile | Asp | Met | Asn | Ala | Arg | Ile | Gly | Lys | Asn | Val | Val | Ile | Thr |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Asn | Ser | Lys | Gly | Ile | Gln | Glu | Ala | Asp | His | Pro | Glu | Glu | Gly | Tyr | Tyr |
| | | | 485 | | | | | | 490 | | | | | 495 | |
| Ile | Arg | Ser | Gly | Ile | Val | Val | Ile | Leu | Lys | Asn | Ala | Thr | Ile | Asn | Asp |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Gly | Ser | Val | Ile | | | | | | | | | | | | |
| | | | 515 | | | | | | | | | | | | |

<210> 21
 <211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (321)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

<400> 21
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
 1 5 10
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

 cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

 agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

 ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

 tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca acn gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
 130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
 145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
 160 165 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
 Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
 175 180 185 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
 Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
 195 200 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675
 Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
 210 215 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct 723
 Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
 225 230 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat 771
 Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
 240 245 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat 819
 His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
 255 260 265 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat 867
 Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
 275 280 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc 915
 Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
 290 295 300

| | |
|---|------|
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |
| 415 420 425 430 | |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | |
| 435 440 445 | |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile | |
| 450 455 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | |
| 465 470 475 | |
| atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg | 1491 |
| Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly | |
| 480 485 490 | |
| tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc | 1539 |
| Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile | |
| 495 500 505 510 | |
| aac gat ggg tct gtc ata tagatcggct gcgktgcg | 1576 |
| Asn Asp Gly Ser Val Ile | |
| 515 | |

<210> 22
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 22

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Met  Gln  Phe  Ala  Leu  Ala  Leu  Asp  Thr  Asn  Ser  Gly  Pro  His  Gln  Ile
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Arg  Ser  Cys  Glu  Gly  Asp  Gly  Ile  Asp  Arg  Leu  Glu  Lys  Leu  Ser  Ile
          20              25              30

Gly  Gly  Arg  Lys  Gln  Glu  Lys  Ala  Leu  Arg  Asn  Arg  Cys  Phe  Gly  Gly
          35              40              45

Arg  Val  Ala  Ala  Thr  Thr  Gln  Cys  Ile  Leu  Thr  Ser  Asp  Ala  Cys  Pro
  50              55              60

Glu  Thr  Leu  His  Ser  Gln  Thr  Gln  Ser  Ser  Arg  Lys  Asn  Tyr  Ala  Asp
  65              70              75              80

Ala  Asn  Arg  Val  Ser  Ala  Ile  Ile  Leu  Gly  Gly  Gly  Thr  Gly  Ser  Gln
          85              90              95

Leu  Phe  Pro  Leu  Thr  Ser  Thr  Thr  Ala  Thr  Pro  Ala  Val  Pro  Val  Gly
          100              105              110

Gly  Cys  Tyr  Arg  Leu  Ile  Asp  Ile  Pro  Met  Ser  Asn  Cys  Phe  Asn  Ser
          115              120              125

Gly  Ile  Asn  Lys  Ile  Phe  Val  Met  Ser  Gln  Phe  Asn  Ser  Thr  Ser  Leu
  130              135              140

Asn  Arg  His  Ile  His  Arg  Thr  Tyr  Leu  Glu  Gly  Gly  Ile  Asn  Phe  Ala
  145              150              155              160

Asp  Gly  Ser  Val  Gln  Val  Leu  Ala  Ala  Thr  Gln  Met  Pro  Glu  Glu  Pro
          165              170              175

Ala  Gly  Trp  Phe  Gln  Gly  Thr  Ala  Asp  Ser  Ile  Arg  Lys  Phe  Ile  Trp
          180              185              190

Val  Leu  Glu  Asp  Tyr  Tyr  Ser  His  Lys  Ser  Ile  Asp  Asn  Ile  Val  Ile
          195              200              205

Leu  Ser  Gly  Asp  Gln  Leu  Tyr  Arg  Met  Asn  Tyr  Met  Glu  Leu  Val  Gln
  210              215              220

Lys  His  Val  Glu  Asp  Asp  Ala  Asp  Ile  Thr  Ile  Ser  Cys  Ala  Pro  Val
  225              230              235              240

Asp  Glu  Ser  Arg  Ala  Ser  Lys  Asn  Gly  Leu  Val  Lys  Ile  Asp  His  Thr
          245              250              255

Gly  Arg  Val  Leu  Gln  Phe  Phe  Glu  Lys  Pro  Lys  Gly  Ala  Asp  Leu  Asn

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| 260 | 265 | 270 |
|---|-----|-----|
| Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala | | |
| 275 | 280 | 285 |
| Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys | | |
| 290 | 295 | 300 |
| Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp | | |
| 305 | 310 | 315 |
| Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln | | |
| | 325 | 330 |
| Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser | | |
| | 340 | 345 |
| Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp | | |
| | 355 | 360 |
| Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro | | |
| | 370 | 375 |
| Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp | | |
| | 385 | 390 |
| Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val | | |
| | 405 | 410 |
| Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met | | |
| | 420 | 425 |
| Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu | | |
| | 435 | 440 |
| Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn | | |
| | 450 | 455 |
| Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr | | |
| | 465 | 470 |
| Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr | | |
| | 485 | 490 |
| Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp | | |
| | 500 | 505 |
| Gly Ser Val Ile | | |
| | 515 | |

<210> 23

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
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 <222> (1389)
 <223> h = a or c or t/u.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

<400> 23

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Ser | Gln | Leu | Phe | Pro | Leu | Thr | Ser | Thr | Arg | Ala | Thr | Pro | Ala | Val | Pro | | |
| 95 | | | | | 100 | | | | | 105 | | | | | 110 | | |
| ggt | gga | gga | tgt | tac | agg | ctt | att | gat | atc | cct | atg | agt | aac | tgc | ttc | 387 | |
| Val | Gly | Gly | Cys | Tyr | Arg | Leu | Ile | Asp | Ile | Pro | Met | Ser | Asn | Cys | Phe | | |
| | | | | 115 | | | | | 120 | | | | | 125 | | | |
| aac | agt | ggt | ata | aat | aag | ata | ttt | gtg | atg | agt | cag | ttc | aat | tct | act | 435 | |
| Asn | Ser | Gly | Ile | Asn | Lys | Ile | Phe | Val | Met | Ser | Gln | Phe | Asn | Ser | Thr | | |
| | | | 130 | | | | | 135 | | | | | 140 | | | | |
| tcg | ctt | aac | cgc | cat | att | cat | cgt | aca | tac | ctt | gaa | ggc | ggg | atc | aac | 483 | |
| Ser | Leu | Asn | Arg | His | Ile | His | Arg | Thr | Tyr | Leu | Glu | Gly | Gly | Ile | Asn | | |
| | | 145 | | | | | 150 | | | | | 155 | | | | | |
| ttt | gct | gat | gga | tct | gta | cag | gta | tta | gcg | gct | aca | caa | atg | cct | gaa | 531 | |
| Phe | Ala | Asp | Gly | Ser | Val | Gln | Val | Leu | Ala | Ala | Thr | Gln | Met | Pro | Glu | | |
| | 160 | | | | | 165 | | | | | 170 | | | | | | |
| gag | cca | gct | gga | tgg | ttc | cag | ggt | aca | gca | gac | tct | atc | aga | aaa | ttt | 579 | |
| Glu | Pro | Ala | Gly | Trp | Phe | Gln | Gly | Thr | Ala | Asp | Ser | Ile | Arg | Lys | Phe | | |
| 175 | | | | | 180 | | | | | 185 | | | | | 190 | | |
| atc | tgg | gta | ctc | gag | gat | tat | tac | agt | cac | aaa | tcc | att | gac | aac | att | 627 | |
| Ile | Trp | Val | Leu | Glu | Asp | Tyr | Tyr | Ser | His | Lys | Ser | Ile | Asp | Asn | Ile | | |
| | | | 195 | | | | | | 200 | | | | | 205 | | | |
| gta | atc | ttg | agt | ggc | gat | cag | ctt | tat | cgg | atg | aat | tac | atg | gaa | ctt | 675 | |
| Val | Ile | Leu | Ser | Gly | Asp | Gln | Leu | Tyr | Arg | Met | Asn | Tyr | Met | Glu | Leu | | |
| | | | 210 | | | | | 215 | | | | | 220 | | | | |
| gtg | cag | aaa | cat | gtc | gag | gac | gat | gct | gat | atc | act | ata | tca | tgt | gct | 723 | |
| Val | Gln | Lys | His | Val | Glu | Asp | Asp | Ala | Asp | Ile | Thr | Ile | Ser | Cys | Ala | | |
| | | 225 | | | | | 230 | | | | | 235 | | | | | |
| cct | gtt | gat | gag | agc | cga | gct | tct | aaa | aat | ggg | cta | gtg | aag | att | gat | 771 | |
| Pro | Val | Asp | Glu | Ser | Arg | Ala | Ser | Lys | Asn | Gly | Leu | Val | Lys | Ile | Asp | | |
| | 240 | | | | | 245 | | | | | 250 | | | | | | |
| cat | act | gga | cgt | gta | ctt | caa | ttc | ttt | gaa | aaa | cca | aag | ggt | gct | gat | 819 | |
| His | Thr | Gly | Arg | Val | Leu | Gln | Phe | Phe | Glu | Lys | Pro | Lys | Gly | Ala | Asp | | |
| 255 | | | | | 260 | | | | | 265 | | | | | 270 | | |
| ttg | aat | tct | atg | aga | gtt | gag | acc | aac | ttc | ctg | agc | tat | gct | ata | gat | 867 | |
| Leu | Asn | Ser | Met | Arg | Val | Glu | Thr | Asn | Phe | Leu | Ser | Tyr | Ala | Ile | Asp | | |
| | | | | 275 | | | | | 280 | | | | | 285 | | | |
| gat | gca | cag | aaa | tat | cca | tac | ctt | gca | tca | atg | ggc | att | tat | gtc | ttc | 915 | |
| Asp | Ala | Gln | Lys | Tyr | Pro | Tyr | Leu | Ala | Ser | Met | Gly | Ile | Tyr | Val | Phe | | |
| | | | 290 | | | | | 295 | | | | | 300 | | | | |
| aag | aaa | gat | gca | ctt | tta | gac | ctt | ctc | aag | tca | aaa | tat | act | caa | tta | 963 | |
| Lys | Lys | Asp | Ala | Leu | Leu | Asp | Leu | Leu | Lys | Ser | Lys | Tyr | Thr | Gln | Leu | | |
| | | 305 | | | | | 310 | | | | | 315 | | | | | |
| cat | gac | ttt | gga | tct | gaa | atc | ctc | cca | aga | gct | gta | cta | gat | tay | agt | 1011 | |
| His | Asp | Phe | Gly | Ser | Glu | Ile | Leu | Pro | Arg | Ala | Val | Leu | Asp | Tyr | Ser | | |

| 320 | 325 | 330 | |
|---|-----|-----|------|
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | | | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | | | |
| 335 | 340 | 345 | 350 |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | | | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | | | |
| | 355 | 360 | 365 |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | | | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | | | |
| | 370 | 375 | 380 |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | | | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | | | |
| | 385 | 390 | 395 |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | | | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | | | |
| | 400 | 405 | 410 |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | | | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | | | |
| | 415 | 420 | 425 |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | | | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | | | |
| | 435 | 440 | 445 |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac ath aag ata | | | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile | | | |
| | 450 | 455 | 460 |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | | | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | | | |
| | 465 | 470 | 475 |
| atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg | | | 1491 |
| Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly | | | |
| | 480 | 485 | 490 |
| tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc | | | 1539 |
| Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile | | | |
| | 495 | 500 | 505 |
| aac gat ggg tct gtc ata tagatcggt gcgktkgcg | | | 1576 |
| Asn Asp Gly Ser Val Ile | | | |
| | 515 | | |

<210> 24

<211> 516

<212> PRT

<213> Zea mays

<400> 24

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1 5 10 15
 Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300

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Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                      310                      315                      320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                      325                      330                      335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                      340                      345                      350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
                      355                      360                      365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
                      370                      375                      380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                      390                      395                      400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                      405                      410                      415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                      420                      425                      430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
                      435                      440                      445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile Arg Asn
                      450                      455                      460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                      470                      475                      480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
                      500                      505                      510

Gly Ser Val Ile
                      515

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<210> 25

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (657)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 25

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1

5

10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
115 120 125

| | |
|---|------|
| aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act | 435 |
| Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr | |
| 130 135 140 | |
| tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac | 483 |
| Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn | |
| 145 150 155 | |
| ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa | 531 |
| Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu | |
| 160 165 170 | |
| gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | 579 |
| Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | |
| 175 180 185 190 | |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | 627 |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | |
| 195 200 205 | |
| gta atc ttg agt ggc gat cag ctt tat ccn atg aat tac atg gaa ctt | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu | |
| 210 215 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | |
| 225 230 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | |
| 240 245 250 | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
 Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
 355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
 370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
 385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 26

<211> 516

<212> PRT

<213> Zea mays

<400> 26

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile

| 20 | | | | | 25 | | | | | 30 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Arg | Lys | Gln | Glu | Lys | Ala | Leu | Arg | Asn | Arg | Cys | Phe | Gly | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Arg | Val | Ala | Ala | Thr | Thr | Gln | Cys | Ile | Leu | Thr | Ser | Asp | Ala | Cys | Pro |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Thr | Leu | His | Ser | Gln | Thr | Gln | Ser | Ser | Arg | Lys | Asn | Tyr | Ala | Asp |
| | 65 | | | | | 70 | | | | | 75 | | | | 80 |
| Ala | Asn | Arg | Val | Ser | Ala | Ile | Ile | Leu | Gly | Gly | Gly | Thr | Gly | Ser | Gln |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Leu | Phe | Pro | Leu | Thr | Ser | Thr | Arg | Ala | Thr | Pro | Ala | Val | Pro | Val | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | Cys | Tyr | Arg | Leu | Ile | Asp | Ile | Pro | Met | Ser | Asn | Cys | Phe | Asn | Ser |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gly | Ile | Asn | Lys | Ile | Phe | Val | Met | Ser | Gln | Phe | Asn | Ser | Thr | Ser | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asn | Arg | His | Ile | His | Arg | Thr | Tyr | Leu | Glu | Gly | Gly | Ile | Asn | Phe | Ala |
| | 145 | | | | | 150 | | | | | 155 | | | | 160 |
| Asp | Gly | Ser | Val | Gln | Val | Leu | Ala | Ala | Thr | Gln | Met | Pro | Glu | Glu | Pro |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Gly | Trp | Phe | Gln | Gly | Thr | Ala | Asp | Ser | Ile | Arg | Lys | Phe | Ile | Trp |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Val | Leu | Glu | Asp | Tyr | Tyr | Ser | His | Lys | Ser | Ile | Asp | Asn | Ile | Val | Ile |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Leu | Ser | Gly | Asp | Gln | Leu | Tyr | Pro | Met | Asn | Tyr | Met | Glu | Leu | Val | Gln |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Lys | His | Val | Glu | Asp | Asp | Ala | Asp | Ile | Thr | Ile | Ser | Cys | Ala | Pro | Val |
| | 225 | | | | | 230 | | | | | 235 | | | 240 | |
| Asp | Glu | Ser | Arg | Ala | Ser | Lys | Asn | Gly | Leu | Val | Lys | Ile | Asp | His | Thr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Gly | Arg | Val | Leu | Gln | Phe | Phe | Glu | Lys | Pro | Lys | Gly | Ala | Asp | Leu | Asn |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ser | Met | Arg | Val | Glu | Thr | Asn | Phe | Leu | Ser | Tyr | Ala | Ile | Asp | Asp | Ala |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Gln | Lys | Tyr | Pro | Tyr | Leu | Ala | Ser | Met | Gly | Ile | Tyr | Val | Phe | Lys | Lys |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asp | Ala | Leu | Leu | Asp | Leu | Leu | Lys | Ser | Lys | Tyr | Thr | Gln | Leu | His | Asp |
| | 305 | | | | | 310 | | | | | 315 | | | 320 | |

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
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 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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 500 505 510
 Gly Ser Val Ile
 515

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<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

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 <222> (540)
 <223> n = a or g or c or t/u, unknown, or other.

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 <222> (1008)
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<222> (1368)
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          1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
          80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

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| 115 | | | | | | | | | | 120 | | | | | | | | | | 125 | | | | | | | | | | |
|---|------|--|--|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act | 435 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 130 135 140 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac | 483 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 145 150 155 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa | 531 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 160 165 170 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | 579 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 175 180 185 190 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | 627 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 195 200 205 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | 675 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 210 215 220 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | 723 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 225 230 235 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | 771 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 240 245 250 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 255 260 265 270 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 275 280 285 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 290 295 300 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 305 310 315 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt | 1011 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 320 325 330 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 335 340 345 350 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
 Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
 355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
 370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
 385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
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gga gtc tgc tca cgt gtc agc tct gga tgt gaa tty aag gac tcc gtg 1299
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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aac gat ggg tct gtc ata tagatcggct gcgktgcg 1576
 Asn Asp Gly Ser Val Ile
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<211> 516

<212> PRT

<213> Zea mays

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Gly | Gly | Arg | Lys | Gln | Glu | Lys | Ala | Leu | Arg | Asn | Arg | Cys | Phe | Gly | Gly | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Arg | Val | Ala | Ala | Thr | Thr | Gln | Cys | Ile | Leu | Thr | Ser | Asp | Ala | Cys | Pro | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Glu | Thr | Leu | His | Ser | Gln | Thr | Gln | Ser | Ser | Arg | Lys | Asn | Tyr | Ala | Asp | |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ala | Asn | Arg | Val | Ser | Ala | Ile | Ile | Leu | Gly | Gly | Gly | Thr | Gly | Ser | Gln | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Leu | Phe | Pro | Leu | Thr | Ser | Thr | Arg | Ala | Thr | Pro | Ala | Val | Pro | Val | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Gly | Cys | Tyr | Arg | Leu | Ile | Asp | Ile | Pro | Met | Ser | Asn | Cys | Phe | Asn | Ser | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Gly | Ile | Asn | Lys | Ile | Phe | Val | Met | Ser | Gln | Phe | Asn | Ser | Thr | Ser | Leu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Asn | Arg | His | Ile | His | Arg | Thr | Tyr | Leu | Glu | Gly | Gly | Ile | Asn | Phe | Ala | |
| | 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Asp | Gly | Ser | Val | Gln | Val | Leu | Ala | Ala | Thr | Gln | Met | Pro | Glu | Glu | Pro | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Val | Gly | Trp | Phe | Gln | Gly | Thr | Ala | Asp | Ser | Ile | Arg | Lys | Phe | Ile | Trp | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Val | Leu | Glu | Asp | Tyr | Tyr | Ser | His | Lys | Ser | Ile | Asp | Asn | Ile | Val | Ile | |
| | 195 | | | | | | 200 | | | | | 205 | | | | |
| Leu | Ser | Gly | Asp | Gln | Leu | Tyr | Arg | Met | Asn | Tyr | Met | Glu | Leu | Val | Gln | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Lys | His | Val | Glu | Asp | Asp | Ala | Asp | Ile | Thr | Ile | Ser | Cys | Ala | Pro | Val | |
| | 225 | | | | | 230 | | | | | 235 | | | 240 | | |
| Asp | Glu | Ser | Arg | Ala | Ser | Lys | Asn | Gly | Leu | Val | Lys | Ile | Asp | His | Thr | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Gly | Arg | Val | Leu | Gln | Phe | Phe | Glu | Lys | Pro | Lys | Gly | Ala | Asp | Leu | Asn | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Ser | Met | Arg | Val | Glu | Thr | Asn | Phe | Leu | Ser | Tyr | Ala | Ile | Asp | Asp | Ala | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Gln | Lys | Tyr | Pro | Tyr | Leu | Ala | Ser | Met | Gly | Ile | Tyr | Val | Phe | Lys | Lys | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Asp | Ala | Leu | Leu | Asp | Leu | Leu | Lys | Ser | Lys | Tyr | Thr | Gln | Leu | His | Asp | |
| | 305 | | | | | 310 | | | | | 315 | | | | 320 | |

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
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 Gly Ser Val Ile
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<210> 29

<211> 1576

<212> DNA

<213> Zea mays

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<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation
 <222> (981)
 <223> r = g or a.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

| 95 | 100 | 105 | 110 | |
|---|-----|-----|-----|------|
| ggt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc | | | | 387 |
| Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe | | | | |
| | 115 | 120 | 125 | |
| aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act | | | | 435 |
| Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr | | | | |
| | 130 | 135 | 140 | |
| tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac | | | | 483 |
| Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn | | | | |
| | 145 | 150 | 155 | |
| ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa | | | | 531 |
| Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu | | | | |
| | 160 | 165 | 170 | |
| gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | | | | 579 |
| Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | | | | |
| | 175 | 180 | 185 | 190 |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | | | | 627 |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | | | | |
| | 195 | 200 | 205 | |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | | | | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | | | | |
| | 210 | 215 | 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | | | | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | | | | |
| | 225 | 230 | 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | | | | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | | | | |
| | 240 | 245 | 250 | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | | | | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | | | | |
| | 255 | 260 | 265 | 270 |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | | | | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | | | | |
| | 275 | 280 | 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | | | | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | | | | |
| | 290 | 295 | 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | | | | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | | | | |
| | 305 | 310 | 315 | |
| cat gac ttt gga tct aar atc ctc cca aga gct gta cta gat cay agt | | | | 1011 |
| His Asp Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser | | | | |
| | 320 | 325 | 330 | |

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335 340 345 350

aaa tca ttc ttt gat gca aac ttg gtn ctc act gag cag cct tcc aag 1107
Lys Ser Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys
355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495 500 505 510

aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1576
Asn Asp Gly Ser Val Ile
515

<210> 30

<211> 516

<212> PRT

<213> Zea mays

<400> 30

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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 Gly Ser Val Ile
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<210> 31

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 31

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        1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
          80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
          95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
          115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
          130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Ser | Leu | Asn | Arg | His | Ile | His | Arg | Thr | Tyr | Leu | Glu | Gly | Gly | Ile | Asn | | |
| | | 145 | | | | | 150 | | | | | 155 | | | | | |
| ttt | gct | gat | gga | tct | gta | cag | gta | tta | gcg | gct | aca | caa | atg | cct | gaa | 531 | |
| Phe | Ala | Asp | Gly | Ser | Val | Gln | Val | Leu | Ala | Ala | Thr | Gln | Met | Pro | Glu | | |
| | 160 | | | | | 165 | | | | | 170 | | | | | | |
| gag | cca | gct | gga | tgg | ttc | cag | ggg | aca | gca | gac | tct | atc | aga | aaa | ttt | 579 | |
| Glu | Pro | Ala | Gly | Trp | Phe | Gln | Gly | Thr | Ala | Asp | Ser | Ile | Arg | Lys | Phe | | |
| 175 | | | | | 180 | | | | | 185 | | | | | 190 | | |
| atc | tgg | gta | ctc | gag | gat | tat | tac | agt | cac | aaa | tcc | att | gac | aac | att | 627 | |
| Ile | Trp | Val | Leu | Glu | Asp | Tyr | Tyr | Ser | His | Lys | Ser | Ile | Asp | Asn | Ile | | |
| | | | | 195 | | | | | 200 | | | | | 205 | | | |
| gta | atc | ttg | agt | ggc | gat | cag | ctt | tat | cgg | atg | aat | tac | atg | gaa | ctt | 675 | |
| Val | Ile | Leu | Ser | Gly | Asp | Gln | Leu | Tyr | Arg | Met | Asn | Tyr | Met | Glu | Leu | | |
| | | 210 | | | | | | 215 | | | | | 220 | | | | |
| gtg | cag | aaa | cat | gtc | gag | gac | gat | gct | gat | atc | act | ata | tca | tgt | gct | 723 | |
| Val | Gln | Lys | His | Val | Glu | Asp | Asp | Ala | Asp | Ile | Thr | Ile | Ser | Cys | Ala | | |
| | 225 | | | | | | 230 | | | | | 235 | | | | | |
| cct | gtt | gat | gag | agc | cga | gct | tct | aaa | aat | ggg | cta | gtg | aag | att | gat | 771 | |
| Pro | Val | Asp | Glu | Ser | Arg | Ala | Ser | Lys | Asn | Gly | Leu | Val | Lys | Ile | Asp | | |
| | 240 | | | | | 245 | | | | | 250 | | | | | | |
| cat | act | gga | cgt | gta | ctt | caa | ttc | ttt | gaa | aaa | cca | aag | ggg | gct | gat | 819 | |
| His | Thr | Gly | Arg | Val | Leu | Gln | Phe | Phe | Glu | Lys | Pro | Lys | Gly | Ala | Asp | | |
| 255 | | | | | 260 | | | | | 265 | | | | | 270 | | |
| ttg | aat | tct | atg | aga | gtt | gag | acc | aac | ttc | ctg | agc | tat | gct | ata | gat | 867 | |
| Leu | Asn | Ser | Met | Arg | Val | Glu | Thr | Asn | Phe | Leu | Ser | Tyr | Ala | Ile | Asp | | |
| | | | | 275 | | | | | 280 | | | | | 285 | | | |
| gat | gca | cag | aaa | tat | cca | tac | ctt | gca | tca | atg | ggc | att | tat | gtc | ttc | 915 | |
| Asp | Ala | Gln | Lys | Tyr | Pro | Tyr | Leu | Ala | Ser | Met | Gly | Ile | Tyr | Val | Phe | | |
| | | 290 | | | | | | 295 | | | | | 300 | | | | |
| aag | aaa | gat | gca | ctt | tta | gac | ctt | ctc | aag | tca | aaa | tat | act | caa | tta | 963 | |
| Lys | Lys | Asp | Ala | Leu | Leu | Asp | Leu | Leu | Lys | Ser | Lys | Tyr | Thr | Gln | Leu | | |
| | 305 | | | | | 310 | | | | | | 315 | | | | | |
| cat | gac | ttt | gga | tct | gaa | atc | ctc | cca | aga | gct | gta | cta | gat | tty | agt | 1011 | |
| His | Asp | Phe | Gly | Ser | Glu | Ile | Leu | Pro | Arg | Ala | Val | Leu | Asp | Phe | Ser | | |
| | 320 | | | | | 325 | | | | | 330 | | | | | | |
| gtg | cag | gca | tgc | att | ttt | acg | ggc | tat | tgg | gag | gat | gtt | gga | aca | atc | 1059 | |
| Val | Gln | Ala | Cys | Ile | Phe | Thr | Gly | Tyr | Trp | Glu | Asp | Val | Gly | Thr | Ile | | |
| 335 | | | | | 340 | | | | | 345 | | | | | 350 | | |
| aaa | tca | ttc | ttt | gat | gca | aac | ttg | gcc | ctc | act | gag | cag | cct | tcc | aag | 1107 | |
| Lys | Ser | Phe | Phe | Asp | Ala | Asn | Leu | Ala | Leu | Thr | Glu | Gln | Pro | Ser | Lys | | |
| | | | | 355 | | | | 360 | | | | | | 365 | | | |
| ttt | gat | ttt | tac | gat | cca | aaa | aca | cct | ttc | ttc | act | gca | ccc | cga | tgc | 1155 | |
| Phe | Asp | Phe | Tyr | Asp | Pro | Lys | Thr | Pro | Phe | Phe | Thr | Ala | Pro | Arg | Cys | | |

| 370 | 375 | 380 | |
|---|-----|-----|------|
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | | | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | | | |
| 385 | 390 | 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | | | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | | | |
| 400 | 405 | 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | | | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | | | |
| 415 | 420 | 425 | 430 |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | | | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | | | |
| 435 | 440 | 445 | |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata | | | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile | | | |
| 450 | 455 | 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | | | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | | | |
| 465 | 470 | 475 | |
| atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg | | | 1491 |
| Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly | | | |
| 480 | 485 | 490 | |
| tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc | | | 1539 |
| Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile | | | |
| 495 | 500 | 505 | 510 |
| aac gat ggg tct gtc ata tagatcggct gcgktgcg | | | 1576 |
| Asn Asp Gly Ser Val Ile | | | |
| 515 | | | |

<210> 32

<211> 516

<212> PRT

<213> Zea mays

<400> 32

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| 1 | 5 | 10 | 15 |
| Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile | | | |
| 20 | 25 | 30 | |
| Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly | | | |
| 35 | 40 | 45 | |
| Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro | | | |
| 50 | 55 | 60 | |

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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 500 505 510
 Gly Ser Val Ile
 515

<210> 33

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 33

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          1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
160             165             170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175             180             185             190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627

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| | |
|---|------|
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | |
| 195 200 205 | |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | |
| 210 215 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | |
| 225 230 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | |
| 240 245 250 | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |

| 415 | 420 | 425 | 430 | |
|---|-----|-----|-----|------|
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | | | | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | | | | |
| | 435 | 440 | 445 | |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata | | | | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile | | | | |
| | 450 | 455 | 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | | | | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | | | | |
| | 465 | 470 | 475 | |
| atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg | | | | 1491 |
| Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly | | | | |
| | 480 | 485 | 490 | |
| tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc | | | | 1539 |
| Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile | | | | |
| 495 | 500 | 505 | 510 | |
| aac gat ggg tct gtc ata tagatcggct gcgktkgcg | | | | 1576 |
| Asn Asp Gly Ser Val Ile | | | | |
| | 515 | | | |

<210> 34

<211> 516

<212> PRT

<213> Zea mays

<400> 34

| | | | |
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| 20 | 25 | 30 | |
| Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly | | | |
| 35 | 40 | 45 | |
| Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro | | | |
| 50 | 55 | 60 | |
| Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp | | | |
| 65 | 70 | 75 | 80 |
| Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln | | | |
| 85 | 90 | 95 | |
| Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly | | | |
| 100 | 105 | 110 | |
| Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser | | | |
| 115 | 120 | 125 | |

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile
 515

<210> 35

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 35

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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
      Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
          80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
          95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
          115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
          130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
          145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
          160             165             170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
          175             180             185             190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
          195             200             205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
          210             215             220

```

| | |
|---|------|
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | |
| 225 230 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | |
| 240 245 250 | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |
| 415 420 425 430 | |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | |
| 435 440 445 | |

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 36
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 36

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
 Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
500 505 510

Gly Ser Val Ile
515

<210> 37

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1197)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 37

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

| 15 | 20 | 25 | 30 | |
|---|-----|-----|-----|-----|
| agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt | | | | 147 |
| Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe | 35 | 40 | 45 | |
| ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct | | | | 195 |
| Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala | 50 | 55 | 60 | |
| tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat | | | | 243 |
| Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr | 65 | 70 | 75 | |
| gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga | | | | 291 |
| Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly | 80 | 85 | 90 | |
| tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct | | | | 339 |
| Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro | 95 | 100 | 105 | 110 |
| gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc | | | | 387 |
| Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe | 115 | 120 | 125 | |
| aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act | | | | 435 |
| Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr | 130 | 135 | 140 | |
| tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac | | | | 483 |
| Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn | 145 | 150 | 155 | |
| ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa | | | | 531 |
| Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu | 160 | 165 | 170 | |
| gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | | | | 579 |
| Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | 175 | 180 | 185 | 190 |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | | | | 627 |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | 195 | 200 | 205 | |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | | | | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | 210 | 215 | 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | | | | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | 225 | 230 | 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | | | | 771 |

| | |
|---|------|
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | |
| 240 245 250 | |
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |
| 415 420 425 430 | |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | |
| 435 440 445 | |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile | |
| 450 455 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | |

| 465 | 470 | 475 | |
|-------------------------|----------------------|---------------------|------|
| atc aca aac agt aag ggc | atc caa gag gct gat | cac ccg gaa gaa ggg | 1491 |
| Ile Thr Asn Ser Lys Gly | Ile Gln Glu Ala Asp | His Pro Glu Glu Gly | |
| 480 | 485 | 490 | |
| tac tac ata agg tct gga | atc gtg gtg atc ctg | aag aat gca acc atc | 1539 |
| Tyr Tyr Ile Arg Ser Gly | Ile Val Val Ile Leu | Lys Asn Ala Thr Ile | |
| 495 | 500 | 505 510 | |
| aac gat ggg tct gtc ata | tagatcggct gcgtktgcg | | 1576 |
| Asn Asp Gly Ser Val Ile | | | |
| 515 | | | |

<210> 38

<211> 516

<212> PRT

<213> Zea mays

<400> 38

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Phe | Ala | Leu | Ala | Leu | Asp | Thr | Asn | Ser | Gly | Pro | His | Gln | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Ser | Cys | Glu | Gly | Asp | Gly | Ile | Asp | Arg | Leu | Glu | Lys | Leu | Ser | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Gly | Arg | Lys | Gln | Glu | Lys | Ala | Leu | Arg | Asn | Arg | Cys | Phe | Gly | Gly |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Arg | Val | Ala | Ala | Thr | Thr | Gln | Cys | Ile | Leu | Thr | Ser | Asp | Ala | Cys | Pro |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Thr | Leu | His | Ser | Gln | Thr | Gln | Ser | Ser | Arg | Lys | Asn | Tyr | Ala | Asp |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ala | Asn | Arg | Val | Ser | Ala | Ile | Ile | Leu | Gly | Gly | Gly | Thr | Gly | Ser | Gln |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Phe | Pro | Leu | Thr | Ser | Thr | Arg | Ala | Thr | Pro | Ala | Val | Pro | Val | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | Cys | Tyr | Arg | Leu | Ile | Asp | Ile | Pro | Met | Ser | Asn | Cys | Phe | Asn | Ser |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Gly | Ile | Asn | Lys | Ile | Phe | Val | Met | Ser | Gln | Phe | Asn | Ser | Thr | Ser | Leu |
| 130 | | | | | 135 | | | | | | 140 | | | | |
| Asn | Arg | His | Ile | His | Arg | Thr | Tyr | Leu | Glu | Gly | Gly | Ile | Asn | Phe | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Asp | Gly | Ser | Val | Gln | Val | Leu | Ala | Ala | Thr | Gln | Met | Pro | Glu | Glu | Pro |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Gly | Trp | Phe | Gln | Gly | Thr | Ala | Asp | Ser | Ile | Arg | Lys | Phe | Ile | Trp |
| | | | 180 | | | | | 185 | | | | | 190 | | |

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile
 515

<210> 39
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 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (540)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
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 <222> (1197)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
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 <222> (1578)
 <223> k = g or t.

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

| | |
|---|-----|
| agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt | 147 |
| Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe | |
| 35 40 45 | |
| ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct | 195 |
| Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala | |
| 50 55 60 | |
| tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat | 243 |
| Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr | |
| 65 70 75 | |
| gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga | 291 |
| Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly | |
| 80 85 90 | |
| tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct | 339 |
| Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro | |
| 95 100 105 110 | |
| gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc | 387 |
| Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe | |
| 115 120 125 | |
| aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act | 435 |
| Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr | |
| 130 135 140 | |
| tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac | 483 |
| Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn | |
| 145 150 155 | |
| ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa | 531 |
| Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu | |
| 160 165 170 | |
| gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt | 579 |
| Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe | |
| 175 180 185 190 | |
| atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att | 627 |
| Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile | |
| 195 200 205 | |
| gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt | 675 |
| Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu | |
| 210 215 220 | |
| gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct | 723 |
| Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala | |
| 225 230 235 | |
| cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat | 771 |
| Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp | |
| 240 245 250 | |

| | |
|---|------|
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |
| 415 420 425 430 | |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | |
| 435 440 445 | |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile | |
| 450 455 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | |
| 465 470 475 | |

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 40

<211> 516

<212> PRT

<213> Zea mays

<400> 40

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp

500

505

510

Gly Ser Val Ile
515

<210> 41

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

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<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 41

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1

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10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Gly | Gly | Arg | Lys | Gln | Glu | Lys | Ala | Leu | Arg | Asn | Arg | Cys | Phe | |
| | | | | 35 | | | | | 40 | | | | | 45 | | |
| ggt | ggt | aga | ggt | gct | gca | act | aca | caa | tgt | att | ctt | acc | tca | gat | gct | 195 |
| Gly | Gly | Arg | Val | Ala | Ala | Thr | Thr | Gln | Cys | Ile | Leu | Thr | Ser | Asp | Ala | |
| | | | 50 | | | | | 55 | | | | 60 | | | | |
| tgt | cct | gaa | act | ctt | cat | tct | caa | aca | cag | tcc | tct | agg | aaa | aat | tat | 243 |
| Cys | Pro | Glu | Thr | Leu | His | Ser | Gln | Thr | Gln | Ser | Ser | Arg | Lys | Asn | Tyr | |
| | | 65 | | | | | 70 | | | | | 75 | | | | |
| gct | gat | gca | aac | cgt | gta | tct | gck | atc | att | ttg | ggc | gga | ggc | act | gga | 291 |
| Ala | Asp | Ala | Asn | Arg | Val | Ser | Ala | Ile | Ile | Leu | Gly | Gly | Gly | Thr | Gly | |
| | 80 | | | | | 85 | | | | | 90 | | | | | |
| tct | cag | ctc | ttt | cct | ctg | aca | agc | aca | aga | gct | acg | cct | gct | gta | cct | 339 |
| Ser | Gln | Leu | Phe | Pro | Leu | Thr | Ser | Thr | Arg | Ala | Thr | Pro | Ala | Val | Pro | |
| | 95 | | | | 100 | | | | 105 | | | | | 110 | | |
| ggt | gga | gga | tgt | tac | agg | ctt | att | gat | atc | cct | atg | agt | aac | tgc | ttc | 387 |
| Val | Gly | Gly | Cys | Tyr | Arg | Leu | Ile | Asp | Ile | Pro | Met | Ser | Asn | Cys | Phe | |
| | | | 115 | | | | | 120 | | | | | | 125 | | |
| aac | agt | ggt | ata | aat | aag | ata | ttt | gtg | atg | agt | cag | ttc | aat | tct | act | 435 |
| Asn | Ser | Gly | Ile | Asn | Lys | Ile | Phe | Val | Met | Ser | Gln | Phe | Asn | Ser | Thr | |
| | | | 130 | | | | 135 | | | | | 140 | | | | |
| tcg | ctt | aac | cgc | cat | att | cat | cgt | aca | tac | ctt | gaa | ggc | ggg | atc | aac | 483 |
| Ser | Leu | Asn | Arg | His | Ile | His | Arg | Thr | Tyr | Leu | Glu | Gly | Gly | Ile | Asn | |
| | | 145 | | | | | 150 | | | | 155 | | | | | |
| ttt | gct | gat | gga | tct | gta | cag | gta | tta | gcg | gct | aca | caa | atg | cct | gaa | 531 |
| Phe | Ala | Asp | Gly | Ser | Val | Gln | Val | Leu | Ala | Ala | Thr | Gln | Met | Pro | Glu | |
| | 160 | | | | | 165 | | | | | 170 | | | | | |
| gag | cca | gtg | gga | tgg | ttc | cag | ggt | aca | gca | gac | tct | atc | aga | aaa | ttt | 579 |
| Glu | Pro | Val | Gly | Trp | Phe | Gln | Gly | Thr | Ala | Asp | Ser | Ile | Arg | Lys | Phe | |
| | 175 | | | | 180 | | | | 185 | | | | | 190 | | |
| atc | tgg | gta | ctc | gag | gat | tat | tac | agt | cac | aaa | tcc | att | gac | aac | att | 627 |
| Ile | Trp | Val | Leu | Glu | Asp | Tyr | Tyr | Ser | His | Lys | Ser | Ile | Asp | Asn | Ile | |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| gta | atc | ttg | agt | ggc | gat | cag | ctt | tat | cgg | atg | aat | tac | atg | gaa | ctt | 675 |
| Val | Ile | Leu | Ser | Gly | Asp | Gln | Leu | Tyr | Arg | Met | Asn | Tyr | Met | Glu | Leu | |
| | | | 210 | | | | | 215 | | | | 220 | | | | |
| gtg | cag | aaa | cat | gtc | gag | gac | gat | gct | gat | atc | act | ata | tca | tgt | gct | 723 |
| Val | Gln | Lys | His | Val | Glu | Asp | Asp | Ala | Asp | Ile | Thr | Ile | Ser | Cys | Ala | |
| | | 225 | | | | 230 | | | | | | 235 | | | | |
| cct | gtt | gat | gag | agc | cga | gct | tct | aaa | aat | ggg | cta | gtg | aag | att | gat | 771 |
| Pro | Val | Asp | Glu | Ser | Arg | Ala | Ser | Lys | Asn | Gly | Leu | Val | Lys | Ile | Asp | |
| | 240 | | | | | 245 | | | | | 250 | | | | | |

| | |
|---|------|
| cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat | 819 |
| His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp | |
| 255 260 265 270 | |
| ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat | 867 |
| Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp | |
| 275 280 285 | |
| gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc | 915 |
| Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe | |
| 290 295 300 | |
| aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta | 963 |
| Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu | |
| 305 310 315 | |
| cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt | 1011 |
| His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser | |
| 320 325 330 | |
| gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc | 1059 |
| Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile | |
| 335 340 345 350 | |
| aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag | 1107 |
| Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys | |
| 355 360 365 | |
| ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc | 1155 |
| Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys | |
| 370 375 380 | |
| ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc | 1203 |
| Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile | |
| 385 390 395 | |
| tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att | 1251 |
| Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile | |
| 400 405 410 | |
| gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg | 1299 |
| Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val | |
| 415 420 425 430 | |
| atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta | 1347 |
| Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu | |
| 435 440 445 | |
| ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata | 1395 |
| Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile | |
| 450 455 460 | |
| agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg | 1443 |
| Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val | |
| 465 470 475 | |
| atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg | 1491 |

Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgtcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 42
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 42

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile
515